



AC- ADD 05334

A<sup>C</sup> - AAD<sup>5</sup>334;

Homo sapiens	Location/Qualifiers
OS	
XX	
Key	
CDS	
FT	
sig_peptide	
FT	
FT	
FT	
mat_peptide	
FT	
FT	
FT	

WO200134626-A1.

XX 01-NOV-2000; 2000WO-US30045.  
PF

PR 05-NOV-1999; 99US-0163581.  
PR 30-JUN-2000; 2000US-0215133.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J;  
XX

DR P-PSDB; AAE01469.  
 XX  
 PT New nucleic acid molecules encoding 28 human secreted proteins for  
 PT diagnosis prevent infection or amelioration medical conditions and  
 PT

xxxi  
useu as docu ammendave o preservave

Claim 1, page 44, 2nd paragraph, line 1-3.

The genes and their secreted proteins are useful for preventing, diagnosing and treating diseases.

Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of

28 genes, based on the tissues in which they are most highly expressed,  
CC and include developing products for the diagnosis or treatment of  
CC

CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.

Gencore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 20:55:43 ; Search time 4666.15 Seconds  
(without alignments)  
6341.443 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 1414 Sequence: 1 agggaccgcgaggaaaggccc.....aaaaaaaaaaaaaaaaaaa 1414

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

```

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_lov:*
6: gb_pat:*
7: gb_ph:*
8: gb_p1:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_urp:*
14: gb_v1:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_v1:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*
```

#### ALIGNMENTS

RESULT 1

AF421380

LOCUS

Homo sapiens anthrax toxin receptor mRNA, complete cds.

DEFINITION

AF421380

ACCESSION

AF421380.1 GI:16566412

VERSION

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrini; Homiridae; Homo.

REFERENCE

1 (bases 1 to 1414)

AUTHORS

Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

TITLE

Identification of the cellular receptor for anthrax toxin

JOURNAL

Nature 414 (6860), 225-229 (2001)

PUBMED

11700562

REMARK

<http://www.nature.com>

2 (bases 1 to 1414)

Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

Direct Submission

Submitted (19-SEP-2001)

Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description		
1	100.0	1414	1414	AF421380	PRI 13-NOV-2001		
2	1193.8	84.4	5540	AF219145	linear mRNA		
3	1052.4	74.4	2112	BC012074	Vertebrata; Euteleostomi; Homo sapiens		
4	890	62.9	1436	AK001463	Homiridae; Homo sapiens		
5	853.4	60.4	5220	AF378762	Mus musculus		
6	542.8	38.4	4007	AK025429	Homo sapiens		
7	255.8	18.1	2126	AK057316	Homo sapiens		
8	236	16.7	1297	BC012475	Homo sapiens		
9	232.2	16.4	2026	AK055636	Homo sapiens		
10	207.8	14.7	1343	AY040326	Homo sapiens		
11	194.4	13.7	81017	AC025010	Homo sapiens		
c	12	194.4	13.7	AC025010	Homo sapiens		
c	13	113	8.0	AK002160	Homo sapiens		
c	14	92.8	6.6	BC003908	Mus musculus		
c	15	62	4.4	AC053530	Homo sapiens		
c	16	61.2	4.3	BC010278	Mus musculus		
c	17	61	4.3	AC10772	Homo sapiens		
c	18	60.2	4.3	AC10772	Homo sapiens		
c	19	60	4.2	67676	AX10488	Mus musculus	
c	20	59.4	4.2	6070	AX281468	Sequence	
c	21	59.4	4.2	6070	AX346804	Sequence	
c	22	59.4	4.2	6070	AX346804	Sequence	
c	23	59.4	4.2	6668	AX345598	Sequence	
c	24	59.4	4.2	13712	AX346333	Sequence	
c	25	59.2	4.2	9219	AX251565	Sequence	
c	26	59.2	4.2	9219	AX347328	Sequence	
c	27	59	4.2	349980	AX345558	Sequence	
c	28	58.4	4.1	74412	AC020767	Homo sapiens	
c	29	58.2	4.1	611	AX187051	Sequence	
c	30	58	4.1	6283	AX345737	Sequence	
c	31	58	4.1	6283	AX348379	Sequence	
c	32	58	4.1	6944	AX347467	Sequence	
c	33	58	4.1	6944	AX349188	Sequence	
c	34	57.8	4.1	7319	AX348494	Sequence	
c	35	57.8	4.1	7736	AF310889	Dictyoste-	
c	36	57.6	4.1	7076	AX347047	AS280003	Sequence
c	37	57.6	4.1	11015	AX281190	Sequence	
c	38	57.6	4.1	11015	AX356159	Sequence	
c	39	57.6	4.1	349980	AX344560	Sequence	
c	40	57.6	4.1	70816	AC101610	Mus muscu-	
c	41	57.2	4.0	349980	AX344556	Sequence	
c	42	57.2	4.0	349980	X544522	D. discoideu-	
c	43	57	4.0	2379	DD31		
c	44	57	4.0	89128	AP001826	Homo sapiens	
c	45	57	4.0	126038	AC016688	Homo sapiens	





OM nucleic - nucleic search, using sw model

Run On: August 9, 2002, 00:23:20 ; Search time 4666.15 Seconds

(without alignments)

4951.169 Million cell updates/sec

Title: US-09-970-076-1\_COPY\_104\_1207

Perfect score: 1104

Sequence: atggccacgcggaggcg...gtggaaaaataaaaaaaa 1104

Scoring table: IDENTITY\_NUC

Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_ltg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_pro:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_yi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_yi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

RESULT 1

AF421380

LOCUS

Homo sapiens

anthrax toxin receptor

mRNA

complete cds.

DEFINITION

AF421380

VERSION

AF421380.1

KEYWORDS

GI:16566412

SOURCE

Homo sapiens

Eukaryota;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

Mammalia;

Eutheria;

Primates;

Catarrhini;

Hominidae;

Homo.

REFERENCE 1

(bases 1 to 1414)

AUTHORS Bradley,K.A.,

Mogridge,J.J.,

Mourez,M.,

Collier,R.J.,

and Young,J.A.T.

TITLE Identification

of the cellular

receptor for anthrax

toxin

JOURNAL Nature

414 (6860),

225-229

(2001)

PUBMED

11700562

REMARK

2 (bases 1 to 1414)

AUTHORS Bradley,K.A.,

Mogridge,J.J.,

Mourez,M.,

Collier,R.J.,

and Young,J.A.T.

TITLE Direct Submission

Submitted (19-SEP-2001)

Department of Oncology, University of

Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA

SUMMARIES

RESULT

No. Score

Query

Match Length

DB

ID

Description

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

AF421380 Homo sapi

AF279145 Homo sapi

BC012074 Homo sapi

AF378762 Mus muscu

AK001463 Homo sapi

AK05429 Homo sapi

AK057316 Homo sapi

BC003908 Mus muscu

AC05010 Homo sapi

AL10155 Homo sapi

AC025010 Homo sapi

I6694 Sequence 14

AC096624 Mus muscu

AF129315 Homo sapi

AC068338 Homo sapi

AC10537 Homo sapi

I6694 Sequence 14

AC096884 Sus scrof

AX083744 Sequence

AF143871 Homo sapi

AC018926 Homo sapi

AC01912 Rattus no

AC016778 Homo sapi

AL626786 Mus muscu

AC005020 Homo sapi

AL359240 Human chr

AC109518 Homo sapi

AC357059 Human DNA

AC105611 Rattus no

AC105642 Rattus no

AL626786 Mus muscu

AC005020 Homo sapi

AC096159 Rattus no

AC007652 Homo sapi

AC008744 Homo sapi

AC008738 Homo sapi

AL450388 Human DNA

AC021798 Homo sapi

AC099065 Homo sapi

AC096542 Homo sapi

AC084217 Mus Muscu



